Conclusions: Among their pts with GI nHl the slow increase of incidence from all lymphoma cases, the slight decrease of MALT lymphomas, the elevation of cases of intestinal and of gastric lymphomas with high grade B-cell origin and at all, in this latter group the beneficial effect of rituximab+CHOP treatment were observed.

P140 **Prognostic impact of 1q21 amplification in patients with multiple myeloma treated by velcade, thalidomide and any conventional chemotherapy**

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Introduction: Amplification of chromosome band 1q21 as well as increased expression of CKS1B gene in this area is a frequently mentioned prognostic factor for patients with multiple myeloma (MM). This study was aimed at comparison of prognostic impact of 1q21 gain in three selected groups of patients with diagnosed MM based on treatment regiment.
Materials and Methods: Plasma cells were identified by cytoplasmic light-chain fluorescence in situ hybridisation (cIg-FISH), 1q21 amplification (Amp1q21) utilizing the 1q21/1p36 DNA probe. Amp1q21 was taken such as detection of one or more additional signals of 1q21. Cut-off level for Amp1q21 was established to 20% of total amount of cells with additional signals detected. Patients with Amp1q21 and patients lacking Amp1q21 of each group were statistically correlated with clinical parameters. Up to date we have carried out analysis of 66 (n = 66) patients. This group of patients with median of follow–up 8.6 months (range: 0.3–30.4) was divided according to the undergone therapy into 3 groups: "C-group" comprises 17 samples of patients treated by any conventional chemotherapy; "T-group" comprises 27 samples of patients treated by thalidomide; "V-group" comprises 22 samples of patients treated by Velcade. The response and other parameters such as time to progression (TTP) and overall survival (OS) were assigned by IMWG criteria.
Results: Amp1q21 was found in 62.1% of all 66 patients. Percentage of patients with Amp1q21 in C/T/V-groups were as follows: 64.7%/40.7%/86.4%, respectively. Clinical parameters valid for patients with Amp1q21 (listed in C/T/V order) were as follows: overall response rate (ORR) 42.8%/83.3%/50%; TTP 8.8/12.1/8.0 months; OS 16.1/6.6/not yet reached for V-group. The same parameters valid for patients lacking Amp1q21: ORR 33.3%/80%/66.7%; TTP not yet reached for C-group/8.2/not yet reached for V-group; OS not yet reached for all groups. TTP median of patients with Amp1q21 vs. patients lacking 1q21 was: 8.2 vs. 12.1 months (p = 0.269), OS 6.6 vs. not yet reached (p = 0.072) in thalidomide group. We did not find any other significant differences between patients with/ without Amp1q21 and their parameters in V- and C-group.
Conclusion: Our results suggest that patients with Amp1q21 treated by thalidomide show a trend towards the worst prognosis based on overall survival. We are currently investigating whether or not our findings will be confirmed on a larger cohort of patients with longer follow-up.
Supported by Monoclonal Gammopathy and Multiple Myeloma Basic Research Centre (LC06027), Masaryk University, Brno, Czech Republic.

P141 **Do the "new drugs" antagonize the impact of unfavourable cytogenetic markers in multiple myeloma?**

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Introduction: In our study, we have concentrated on four aberrations in multiple myeloma (MM) malignant plasma cells: deletions of tumor suppressor genes RB (locus 13q14) and p53 (17q13), translocation involving IGH gene t(4;14), and actually focused amplification of CKS1B gene in 1q21 locus. All of these aberrations are known as negative prognostic factors in patients (pts) treated by conventional therapy or stem cell transplantation. The aim of this study is to show if these selected aberrations act as negative prognostic factors also in patients treated by Velcade or by thalidomide, new drugs used in relapsed patients.
Materials and Methods: We have an increasing group of (recently 42) MM patients. Overall clinical characteristics of the patients at the start of treatment: Average age 63.7 years (SD = 9.4), 57% (24) of men. 12% (5/42 pts) were in stage IA, 26% (11/42 pts) were in stage IIA, 60% (25/42 pts) were in stage IIIA and 2% (1 patient) was in stage IIIB. 69% (29/42 pts) were in first relapse, 24% (10/42 pts) were in second relapse and the other 7% (3/42 pts) were in third relapse. 85% (36/42) pts received at least four cycles of therapy. 64% (27/42) pts reached overall response (OR) during the follow-up (average follow-up was 11.0 months, SD = 5.3 months). For identification of malignant plasma cells in bone marrow samples, we use cytoplasmic immunoglobulin (cIg) labeling methodology (Ahmann et al. 1998). This method allows us to identify simultaneously monotypic plasma cells by monoclonal antibody fluorescence (anti-κ or anti-λ) and to detect chromosomal abnormalities by FISH (cIg-FISH).
Results: Cytogenetic findings: Deletion of RB gene was found in 57% (21/37) of successfully examined patients, deletion of p53 gene was in 53% (17/32) pts, translocation t(4;14) was in 61% (22/36) pts and amplification of 1q21 was in 65% (22/34) pts.
Statistical comparison of clinical response in patients with or without each aberration: We have found no significant difference when compared overall survival (OS), time to progression (TTP), progression-free survival (PFS), duration of response (DOR) and overall response in subgroups of patients with and without of any selected aberration.
Conclusion: In our group of patients, no one of monitored aberrations seems to have any impact, neither positive nor negative, on efficiency of used treatment. It is possible that new drugs, Velcade and thalidomide, antagonize the impact of cytogenetic negative prognostic factors in relapsed patients with MM. However, we will continue in this research to reach larger data set to confirm or disconfirm our results. If this data will be confirmed on larger group of patients, it looks necessary to find other chromosomal abnormalities, relevant for prediction of the prognosis in these patients.
Supported by Myeloma Basic Research Centre Brno MU (LC 06027).

P142 **Factors determining survival in Nigerian patients with lymphoma**

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Background: A diagnosis of malignant lymphomas is increasingly being made in several developing countries making it more imperative for us to analyse the variables that determine

survival in our population. We therefore set out to examine the demographic distribution of our patient population and impact of these factors on morbidity and mortality.
Patients and Methods: We examined retrospectively the outcome of 44 consecutive patients (30 males, 14 females) with Hodgkin's and Non-Hodgkin's lymphoma (HL, NHL) who were seen at our hospital between 04/1999 and 02/2006.
Results: The median age was 33 years (range, 4–73). Of the patients with HL (n = 14, 32%); four (29%), five (36%) and four (29%) respectively had lymphocyte predominant, mixed cellularity and nodular sclerosis while seven (23%) and 24 (77%) of those with NHL (n = 30, 68%) had low-grade and high-grade histology. At presentation 31 of 33 (94%) patients were clinically advanced (stage < 3). Two of the 25 patients screened for HIV antibodies were reactive.
All patients were scheduled to receive chemotherapy. COPP (cyclophosphamide, vincristine, procarbazine and prednisolone; 2–6 cycles) was administered to 11 patients with HL while one had ABVD (doxorubicin, bleomycin, vinblastine and darcabazine). Most of those with NHL had 1–8 cycles of either CVP (cyclophosphamide, vincristine and prednisolone; n = 8) or CHOP (cyclophosphamide, doxorubicin, vincristine and prednisolone; n = 18). Three paediatric patients with aggressive NHL had either COM (cyclophosphamide, vincristine and methotrexate, plus intrathecal therapy; n = 2) or COAP (cyclophosphamide, vincristine, cytosine arabinoside and methotrexate). Overall, 24 (59%) patients had between one and five cycles while 17 (41%) had six or more cycles of chemotherapy.
As of February 2006, 33 patients (79%) remain alive after a median follow-up of 133 days (range, 2–1196) post-therapy; with 9 having died. Overall survival (OS) at 3 years after treatment was 66%. Kaplan–Meier univariate analysis showed a survival advantage of HL over NHL, female over male sex and $\geqslant$6 over <6 chemotherapy cycles.
Conclusion: Our data suggests that despite high default rates, up to 79% short-term survival can be achieved in patients with clinically advanced malignant lymphoma in developing countries. Results are likely to improve with earlier presentation, lower default rates and improvements in chemotherapy support services.

P143 Expression of MAGE-A1 and MAGE-A3 in bone marrow of patients with multiple myeloma

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Introduction: Multiple myeloma (MM) is a malignant plasma cell neoplasm that often is preceded by a common pre-malignant monoclonal expansion of plasma cells called monoclonal gammopathy of undetermined significance (MGUS). MGUS is reported to be present in 1% of the adult population and to progres to MM at a rate of 1% per year. MM is an incurable tumor characterized by clonal expansion of malignant plasma cells in the bone marrow. The MAGE genes encode antigenic peptides that are presented by HLA class I molecules and that are recognized on human tumors by T lymphocytes. They are activated in a variety of malignant neoplasma while remaining silent in normal tissues with the exception of testis and ocassionally placenta. Presence of mRNA transcripts encoding members of the MAGE gene family in myeloma tumor cells and cell lines has been documented. The aim of this study is to evaluate the possibility of using these genes as molecular markers of the progression MGUS to multiple myeloma and the early relapse of the MM. This abstract covers our pilot and preliminary results.
Materials and Methods: Total of 151 samples from bone marrow were evaluated: 83 samples from myeloma patients, 12 samples of patients with early stage of MM who did not require treatment (smoldering MM 4×, stage IA 8×), 41 samples of MGUS patients, 15 samples of normal healthy donors served as control group. Total RNA was evaluated by RT-PCR and then by real-time PCR using FRET probes on the LightCycler instrument (Roche). For relative quantification we used G6PDH housekeeping gene as external standard. As positive control we used myeloma cell line U266.
Results: None from samples of 15 healthy donors did show expression of MAGE. Only 2 of 41 (4.8%) samples from MGUS patient showed expression of MAGE-A1. Six (50%) from 12 patients with early stage of MM (IA and smoldering) showed expression of MAGE. In the group of MM patients 31 (37.3%) of 83 samples showed expression of at least one gene MAGE-A1 or MAGE-A3 or both (20 cases).
Conclusion: We have confirmed that expression of MAGE is not present in samples of healthy donors. There is an obvious correlation between expression of the MAGE genes and early-late stage of the disease as our preliminary evaluation confirmed the detection of low expression levels of MAGE-type mRNA in bone marrow from patients with MGUS and early stage of MM. It is possible that MAGE antigen monitoring may predict the evolution towards more advanced disease as well as this method should be used for monitoring minimal residual disease in patients with MM. The prospective evaluation is under way.
This work is supported by grant of the Ministry of Education, Czech Republic, LC06027.

P144 Cutaneous vasculitis as an initiating paraneoplastic symptom in Hodgkin's lymphoma

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Introduction: Skin vasculitis may associate with infections and autoimmune diseases. Drugs also may induce its presence. Furthermore, vasculitis may appear as paraneoplastic symptom.
Materials and Methods: case report.
Results: A 19 year-old male patient was examined with swollen ankle, knee, elbow and papules presented on lower extremities. Laboratory results showed high erythrocyte sedimentation ratio, positive C reactive protein, increased number of leukocytes and high circulating immune complex level. Histopathology of skin biopsy specimen proved vasculitis. Anti-neutrophil cytoplasmic antibody was not present. Only skin symptoms could be observed, which disappeared on 0.5 mg/bwkg methyl-prednisolon therapy. Few weeks later besides fever and weight loss enlarged cervical lymph nodes developed. Biopsy indicated the presence of mixed cellularity type of Hodgkin's lymphoma. Appropriate examinations revealed stage III/B with favourable prognosis (IPS = 2). Complete remission confirmed with FDG PET was achieved by 8 cycles polychemotherapy (consisted of adriablastin, bleomycine, vinblastin, dacarbasine). Using this therapeutic regime Hodgkin's lymphoma and vasculitis also disappeared.
Conclusion: Present case report indicates the importance of careful examination of patients with cutaneous vasculitis to exclude the presence of other diseases that may stand at the background, including malignant disorders. The diagnosis of such disease has therapeutic consequences. Treatment of the primary lymphoma also results the improvement of secondary skin vasculitis.